

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: August 13, 2003, 04:28:29 / Search time 3057.14 Seconds

(without alignments)
11440.147 Million cell updates/sec

Title: US-09-818-143-6

Perfect score: 1439

Sequence: 1 gagatcccttcgttaatca.....agaaaaaaaaaaaaaa 1439

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues 45562784

1 number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

EST:
1: em_estbda.*
2: em_estbhm.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estio.*
8: em_hrc.*
9: gb_estci.*
10: gb_estc2.*
11: gb_hrc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
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21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vtl.*
28: gb_gss.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1439	100.0	1439	10	AM888220 MKRA3 Hum
2	1292	89.8	2310	11	BC032745 Homo sapi
3	813.6	56.5	922	9	AL521507 AL521507
4	804.6	55.9	922	9	AL521506 AL521506

Result No.	Score	Query Match	Length	DB ID	Description
5	735.2	51.1	741	14	CA430710 UI-H-FH1
6	706	49.1	738	10	BG748266
7	701.4	48.7	703	12	B0009860 UI-H-ED1
8	698.8	48.6	703	12	BM980547
9	698.6	48.5	731	14	CB851585
10	693.6	48.2	1064	14	BX325388
11	687	47.7	703	10	BG678659
12	677.4	47.1	733	12	BM974268
13	655.2	44.1	674	14	CA440929
14	626.6	43.5	668	12	BM701957
15	624.8	43.4	673	13	BQ448042
16	624.8	43.4	683	13	BQ627928
17	607	42.2	760	13	BU170946
18	603.6	41.9	664	12	BM955652
19	596	41.4	766	14	CD104758
20	590.4	41.0	636	13	BU729623
21	582.6	40.5	602	13	BU683800
22	574.4	39.9	594	14	CB052399
23	560.2	38.9	628	9	AA115295
24	555.6	38.6	574	14	CA777565
25	543.6	37.8	605	14	CA777311
26	541	37.6	587	14	CB306370
27	537.6	37.4	571	12	BM710342
28	537	37.3	571	12	BM90782
29	534.6	37.2	542	12	BQ019900
30	532	37.0	540	12	BM090553
31	527	36.6	535	9	AL049024
32	526	36.6	538	10	BF724489
33	525.8	36.5	642	12	BM671762
34	522	36.3	566	13	BU633007
35	517.4	36.0	530	9	AA625435
36	507	35.2	508	14	CA951879
37	504	35.0	558	9	AI983849
38	499.8	34.7	649	10	BE965809
39	496.6	34.5	570	10	AM63887
40	496.2	34.5	501	9	AA780019
41	494	34.3	621	14	W84522
42	483.2	33.6	516	9	AA873315
43	479.2	33.3	518	12	BM984490
44	476.6	33.1	501	9	AM069314
45	476	33.1	479	9	AI926527

ALIGNMENTS

RESULT 1
LOCUS AM888220 1439 bp mRNA linear EST 05-MAR-2001
DEFINITION MKRA3 Human matrix cleavage expression library Homo sapiens cDNA
clone incyte 156751 similar to MKRA3 Matrix remodeling associated
gene 3, mRNA sequence.

ACCESSION AM888220
VERSION AM888220.1 GI:8050231

KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1439)

AUTHORS Walker, M.G. and Vollmuth, W.

TITLE Matrix-remodeling associated genes identified by co-expression

JOURNAL Unpublished
Contact: Michael Walker

Incyte Genomics
3160 Porter Drive, Palo Alto, CA 94304, USA

TELE 650 845-5771
FAX 650 621 8514
Email: mwalker@incyte.com.

FEATURES
source 1. 1439
/organism="Homo sapiens"
/mol_type="mRNA"

Wed Aug 13 15:18:50 2003

UB-09-818-143-6.rst

Page 2

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/db xref="taxon:9606"
/clone="Incye 1556751"
/clone_lib="Human matrix clease expression library"
BASE COUNT      392 a      336 c      373 t
ORIGIN

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Query Match	100.0%	Score 1439;	DB 10;	Length 1439;
Best Local Similarity	100.0%;	Pred. No. 4e-208;		
Matches 1439;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible][illegible]

RESULT 2			
BC032745	EC032745	2310 bp	mRNA
LOCUS			linear
DEFINITION	Homo sapiens, DKFZP434N161 protein, clone	IMAGE:5574690,	mRNA.
ACCESSION	BC032745		
VERSION	BC032745.1	GI:22749759	
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2310)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-0UN-2002) National Institutes of Health, Mammalian		

REMARK COMMENT	NIH-MGC Project URL: http://mgc.ncl.nih.gov Contact: MGC help desk

Email: csapabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mcgmchgt.nih.gov
Akheri N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dierlich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaas, R.,
Maduro, Q.L., Mastello, C., Maskell, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stentrop, S., Thomas, P.J., Touchman, J.W.,
Taugen, C., Vogt, J.L., Walker, M.A., Wecherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2003, 05:31:01 / Search time 321.205 Seconds

(Without alignments)
10025.973 Million cell updates/sec

Title: US-09-818-143-6

Perfect score: 1439

Sequence: 1 ggcgtacccttgcgttaccatca.....agaaaaaataaaaaa 1439

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1504479 seqs, 1118970152 residues

1 number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_NEW_PUB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1439	100.0	1439	9	US-09-818-143-6
2	1439	100.0	1439	10	US-09-974-298-448
3	1257.6	87.4	1324	14	US-10-125-237-4
4	1257.6	87.4	1324	14	US-10-105-891-4
5	629.8	43.8	633	10	US-09-864-864-159
6	562	39.1	562	14	US-10-106-698-427
7	405.8	28.2	495	11	US-09-918-985-22094
8	386.4	26.8	565	10	US-09-833-381-1144
9	386.4	26.8	386	11	US-09-822-846-10
10	355.4	24.7	396	11	US-09-918-995-7821
11	300.4	20.9	309	10	US-09-954-456-1950
12	242.2	16.8	268	10	US-09-833-381-1143
13	188.6	13.1	303	10	US-09-783-590-1803
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15	129.8	9.0	517	10	US-09-833-381-1145
16	118	8.2	196	10	US-09-783-590-4264

17	50.4	3.5	487	13	US-10-027-632-77534	Sequence 77534, A
18	48.4	3.4	40267	11	US-09-978-244A-25	Sequence 25, Appl
19	48.2	3.3	1503841	9	US-09-795-668-1	Sequence 1, Appl1
20	48.2	3.3	1503841	9	US-09-795-668-1	Sequence 1, Appl1
21	48.2	3.3	1503841	10	US-09-946-807-1	Sequence 379, App
22	48	3.3	32189	9	US-09-764-878-379	Sequence 379, App
23	48	3.3	32189	14	US-10-079-854-379	Sequence 379, App
24	48	3.3	32221	9	US-09-764-878-377	Sequence 377, App
25	48	3.3	32221	14	US-10-079-854-377	Sequence 377, App
26	47.8	3.3	518	13	US-10-027-632-14744	Sequence 14744, A
27	47.8	3.3	518	13	US-10-027-632-14745	Sequence 14745, A
28	47.8	3.3	518	13	US-10-027-632-14746	Sequence 14746, A
29	47.8	3.3	518	13	US-10-027-632-14747	Sequence 14747, A
30	47.6	3.3	7597	12	US-10-311-455-985	Sequence 985, App
31	47.6	3.3	32846	12	US-10-017-161-1657	Sequence 1657, App
32	47.2	3.3	483	13	US-10-027-632-40348	Sequence 40348, A
33	47	3.3	11832	9	US-09-037-657-38	Sequence 38, Appl
34	47	3.3	30175	9	US-09-738-878-3	Sequence 3, Appl1
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36	46.8	3.3	1006	13	US-10-027-632-273001	Sequence 273001, A
37	46.2	3.2	68	11	US-09-852-903C-17	Sequence 17, Appl
38	46.2	3.2	591	13	US-10-027-632-24348	Sequence 24348, A
39	46.2	3.2	725	13	US-10-027-632-130534	Sequence 130534, A
40	46	3.2	3768	10	US-09-969-708-464	Sequence 464, App
41	46	3.2	3768	10	US-09-954-531-164	Sequence 164, App
42	46	3.2	3768	10	US-09-954-531-373	Sequence 373, App
43	46	3.2	3768	12	US-09-873-319-689	Sequence 689, App
44	46	3.2	3768	12	US-09-960-706-1041	Sequence 1041, Ap
45	46	3.2	32816	9	US-09-729-094-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-09-818-143-6

Sequence 6, Application US/09818143

Patent No. US20020019000A1

GENERAL INFORMATION:

APPLICANT: Walker, Michael G.

APPLICANT: Volkman, Wayne

APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES

FILE REFERENCE: PB-0004 CIP

CURRENT APPLICATION NUMBER: US/09/818,143

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PERL Program

SEQ ID NO 6

LENGTH: 1439

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: -

OTHER INFORMATION: 1556751CB1

US-09-818-143-6

Query Match 100.0%; Score 1439; DB 9; Length 1439;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAGTACCCCTGTTATTCATCTTTGTGTTAAAGACACCTTGGTGTGCTTCA 60

QY 61 TTCTTGAAGATTAGCCCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCA 120

DB 61 TTCTTGAAGATTAGCCCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCA 120

QY 121 AGAAGAAAAAGAGACAAATTCACCAAAACCCCTCCCTCCCAATGAGAGCCCTGG 180

DB 121 AGAAGAAAAAGAGACAAATTCACCAAAACCCCTCCCTCCCAATGAGAGCCCTGG 180

QY 181 CAAATGTTATTTCTTCAAGAAATCTTCAAGACCTGAAAGCAAGAAAGATTCGCT 240

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Page 2

Db 181 CAAAGTTAAATTTCTGAGAAATCTTCAAGCTGAAAGCGAGAAATATGCT 240
Qy 241 CTGAGGAGCTTGTGCTCCCGCGAGAGCCCGAGAGCTTAAAGTCAAGAGGCGCTCT 300
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Db 1381 TTTAGAGGTAAACAAATTTAATTAAGTACCATTAATGAGAGAGAGAGAGAGAGAGAG 1439

RESULT 2
US-09-974-298-148
Sequence 148, Application US/09974298
Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chem. Hucl-Mel
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 148
LENGTH: 1439
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1556751CB1
US-09-974-298-148

Query Match 100.0%; Score 1439; DB 10; Length 1439;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATCCCTGTTTAAATCACTTTTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 GAGATCCCTGTTTAAATCACTTTTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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Db 61 TTTCTTGAAGAGTAAAGCTGCTGCTCACTTTCACTTAATTTCTCTCTGTCTCAAGAA 120
Qy 121 AGAAG 180
Db 121 AGAAG 180
Qy 181 CAAAGTTAAATTTCTTAAAGAAATCTTCAAGCTGAAAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 CAAAGTTAAATTTCTTAAAGAAATCTTCAAGCTGAAAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 CTGAGGAGGCTTGTGCTCCCGCGAGAGCCCGAGAGCTTAAAGTGAATGCTGCTCT 300
Db 241 CTGAGGAGGCTTGTGCTCCCGCGAGAGCCCGAGAGCTTAAAGTGAATGCTGCTCT 300
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Db 361 GTTGGCAAAACGAGAGGCGGCTCCCAAAACCCCATGTGTGATCAATTAAGTTGGCC 420
Qy 421 GTCCCAAGGCTCCAGCGCAAACTTAAAGAGAGAGGCTTGGTAAACCAAACTGG 480
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Qy 481 GCCAGCTGGGCTTTTAAACCTTGAAGACTTTCGAGCTGCTGAAACAGAGCTGCG 540
Db 481 GCCAGCTGGGCTTTTAAACCTTGAAGACTTTCGAGCTGCTGAAACAGAGCTGCG 540

b6
b7C

3729 CCCCCCTGCTCCATTTTCCCCCCCCCCCCCCCCCC 3780

PA (INCY-) INCYTE PHARM INC.

XX Walker MG, Volkmutz W, Klingler TM;

XX WPI; 2000-317934/27.

XX P-PSDB; AAV70744.

XX Protein co-expressed with matrix-remodeling proteins, useful in the
XX diagnosis and treatment of cancer, cardiomyopathy, arthritis,
XX angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and
XX ulceration.

XX Claim 1; Page 40-41; 55pp; English.

XX The present sequence is NSEQ gene that is co-expressed with one or more
XX known matrix-remodeling genes in a number of biological samples using an
XX expression vector. This sequence was identified from the
XX Incyte clone 1556751. The gene, protein, and antibody sequences can be
XX used in the diagnosis, and treatment or prevention of a disease
XX associated with its altered expression. The diseases that can be treated
XX are matrix-remodeling diseases, including cancer, cardiomyopathy,
XX arthritis, angiogenesis, diabetic necrosis, atherosclerosis, fibrosis,
XX and ulceration.

XX Sequence 1439 BP; 392 A; 336 C; 338 G; 373 T; 0 other;

XX Query Match 100.0%; Score 1439; DB 21; Length 1439;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	GATATACCTTGTATTAACCTTTTGTGTTAAAGACCTTTGGGTCACTGCTCA	60
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DB	121	AGAAAGAAAAAGAGACAAATTTACCGAAGAACCCCTCCCTCCCAAGAGAGCTTGG	180
QY	181	CAATGTATTTTCTTGAAGAAATCTTCAAGACTGAAAGAGCAAGAAAGATCGCT	240
DB	181	CAATGTATTTTCTTGAAGAAATCTTCAAGACTGAAAGAGCAAGAAAGATCGCT	240
QY	241	CTCAGAGGTGGCTTCTGAGTCCCGCGCGCCAGAGCCCAAGTATGTCAGAGGCGCT	300
DB	241	CTCAGAGGTGGCTTCTGAGTCCCGCGCGCCAGAGCCCAAGTATGTCAGAGGCGCT	300
QY	301	GTTCCTCCCGCGGAGCTCAAAATTTCTTCTCAAGAAAGAAACAGGGCATGCGCT	360
DB	301	GTTCCTCCCGCGGAGCTCAAAATTTCTTCTCAAGAAAGAAACAGGGCATGCGCT	360
QY	361	GTTCGCAAAACGAGCGGCGGCTCCGAAAGAACCCCATGTGTGATTAAGTTGGCC	420
DB	361	GTTCGCAAAACGAGCGGCGGCTCCGAAAGAACCCCATGTGTGATTAAGTTGGCC	420
QY	421	GTCCCGAGGCTCCCGAGGCAACTTAAGAGACGGGCTTGTGAAAAACCAACATGG	480
DB	421	GTCCCGAGGCTCCCGAGGCAACTTAAGAGACGGGCTTGTGAAAAACCAACATGG	480
QY	481	GGCAGCTGGGCTTTTAAACCTAGAGACTTCCGAGTGCCTGGAACAGAGCTCGG	540
DB	481	GGCAGCTGGGCTTTTAAACCTAGAGACTTCCGAGTGCCTGGAACAGAGCTCGG	540
QY	541	GGAAACGGGGCTTCCAGAGACACTCAAGTTCTTCAATGAGCTGTTTGGTCCCTAA	600
DB	541	GGAAACGGGGCTTCCAGAGACACTCAAGTTCTTCAATGAGCTGTTTGGTCCCTAA	600
QY	601	GAATTCGACATATGTCTTCTTGTGCTTTCTTGTGAGCAACGAAAGGAGG	660
DB	601	GAATTCGACATATGTCTTCTTGTGCTTTCTTGTGAGCAACGAAAGGAGG	660

QY	661	GTCCAGAGCTCTAAAGAAATGTGCTTGTGATGACAGAGTCCGTCGAAACCAATAGGCC	720
DB	661	GTCCAGAGCTCTTAAGAAATGTGCTTGTGATGACAGAGTCCGTCGAAACCAATAGGCC	720
QY	721	GCTGCTTTTGAAGGCGAGAGTCAAGCTCCAGGCTTTTAAAGCAATTTACAGAG	780
DB	721	GCTGCTTTTGAAGGCGAGAGTCAAGCTCCAGGCTTTTAAAGCAATTTACAGAG	780
QY	781	AGAAAGGCTGAGAGCTGCAAGTTCATTAAGAGCAAGGCTGTTCTCTCTTA	840
DB	781	AGAAAGGCTGAGAGCTGCAAGTTCATTAAGAGCAAGGCTGTTCTCTCTTA	840
QY	841	GAAGAGGCTGAGAGCTGCAAGTTCATTAAGAGCAAGGCTGTTCTCTCTTA	900
DB	841	GAAGAGGCTGAGAGCTGCAAGTTCATTAAGAGCAAGGCTGTTCTCTCTTA	900
QY	901	GTAAGTAAACAAATAGAGGCTTGTGCTGCAAGAGCAAGAGATGATGATGA	960
DB	901	GTAAGTAAACAAATAGAGGCTTGTGCTGCAAGAGCAAGAGATGATGATGA	960
QY	961	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020
DB	961	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020
QY	1021	ACAAACCAAGCTGATGGAACCAATTAATGTGGGTGTGAGAGGAGAGTCCAGC	1080
DB	1021	ACAAACCAAGCTGATGGAACCAATTAATGTGGGTGTGAGAGGAGAGTCCAGC	1080
QY	1081	TTTGGGCACTTTGAGAGCGGTACAAAGGTTCTGTGCTGTGTCTGACCTCGAGC	1140
DB	1081	TTTGGGCACTTTGAGAGCGGTACAAAGGTTCTGTGCTGTGTCTGACCTCGAGC	1140
QY	1141	AGCAGTGAATTTATTTAAGCTTGAAGCAATCTTGTGCGCGAGAGATGATGATG	1200
DB	1141	AGCAGTGAATTTATTTAAGCTTGAAGCAATCTTGTGCGCGAGAGATGATGATG	1200
QY	1201	CTGAGTGGTTCAGAGCATCTTCTCACTTCTTCTGCGTGGATATGAGTCTGTG	1260
DB	1201	CTGAGTGGTTCAGAGCATCTTCTCACTTCTTCTGCGTGGATATGAGTCTGTG	1260
QY	1261	CCTGCGGCGCATCTCTCTCAAGCATATCGATGAGCTTAACTTCACTTCTGATC	1320
DB	1261	CCTGCGGCGCATCTCTCTCAAGCATATCGATGAGCTTAACTTCACTTCTGATC	1320
QY	1321	GATAGCTCATTAAGCCAGATTAATTAAGTATTTTGTGTAATCGTTT	1380
DB	1321	GATAGCTCATTAAGCCAGATTAATTAAGTATTTTGTGTAATCGTTT	1380
QY	1381	TTTGAAGGTAAACAAATTTAATTAAGCTTCACTTAATTAAGAGAGAGAGAGAG	1439
DB	1381	TTTGAAGGTAAACAAATTTAATTAAGCTTCACTTAATTAAGAGAGAGAGAGAG	1439

RESULT 2

AL42450 standard; DNA; 1439 BP.

AL42450;

11-JUL-2002 (first entry)

Human matrix-remodeling-associated nucleotide 6.

Human; ds; matrix-remodeling gene; extracellular matrix; gene;

matrix-remodeling-associated nucleotide; screening; angiogenesis; arthritis;

atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;

Human sapiens.

Key Location/Qualifiers

CDS 168..467
 FT /*tag= a
 PT /product= "Human matrix-remodeling-associated protein 2"
 XX US2002019000-A1.
 XX 14-FEB-2002.
 XX 26-MAR-2001; 2001US-0818143.
 XX 09-OCT-1993; 98US-0169289.
 XX (WALKER) WALKER M G.
 XX (VOLK) VOLK M W.
 XX (KLING) KLINGLER T M.
 XX Walker MG, Volk M W, Klingler TM,
 XX WPI; 2002-338319/37.
 XX P-PSDB; AAO14785.
 DR
 New isolated polynucleotide coexpressed with matrix-remodeling genes,
 PT useful in diagnosis, prognosis, prevention and treatment of diseases
 PT associated with matrix-remodeling such as angiogenesis, arthritis and
 PT cancer
 XX
 XX Claim 1, Page 21, 63pp; English.
 CC The invention comprises human nucleotide sequences which are co-expressed
 CC with matrix-remodeling genes. Matrix-remodeling is associated with the
 CC construction, destruction and reorganization of extracellular matrix
 CC components. The matrix-remodeling-associated nucleotides of the invention
 CC are useful for screening for and purifying ligands that specifically bind
 CC to the nucleotides of the invention. The matrix-remodeling-associated
 CC nucleotides of the invention are also useful in the diagnosis, prognosis,
 CC prevention, treatment and evaluation of therapies for diseases associated
 CC with matrix remodeling (e.g. angiogenesis, arthritis, atherosclerosis,
 CC cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The
 CC present, DNA sequence represents a human matrix-remodeling-associated
 CC nucleotide of the invention.
 CC
 CC Sequence 1439 BP; 392 A; 336 C; 338 G; 373 T; 0 other;
 SQ
 Query Match 100.0%; Score 1439; DB 24; Length 1439;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GAGTATCCCTGTTTAACTCTTTGTGTAAAGAGACCTTGGGTGAGTCTGCTCA 60
 1 GAGTATCCCTGTTTAACTCTTTGTGTAAAGAGACCTTGGGTGAGTCTGCTCA 60
 61 TTCTTGAAGAGTTAGCCCTGCTCACTTTCACTTATTTCTCCGTCTCAAGAA 120
 61 TTCTTGAAGAGTTAGCCCTGCTCACTTTCACTTATTTCTCCGTCTCAAGAA 120
 121 AAGAGAAAAAGAGCAATTCAGCAAAACCTCTCCCTCCCAATGAGGCTTGG 180
 121 AAGAGAAAAAGAGCAATTCAGCAAAACCTCTCCCTCCCAATGAGGCTTGG 180
 121 AAGAGAAAAAGAGCAATTCAGCAAAACCTCTCCCTCCCAATGAGGCTTGG 180
 121 AAGAGAAAAAGAGCAATTCAGCAAAACCTCTCCCTCCCAATGAGGCTTGG 180
 181 CAAATGTTAATTTCTTGAAGAAATCCTTCAAGCTGAGAGAGAGAAATCTGCT 240
 181 CAAATGTTAATTTCTTGAAGAAATCCTTCAAGCTGAGAGAGAGAAATCTGCT 240
 181 CAAATGTTAATTTCTTGAAGAAATCCTTCAAGCTGAGAGAGAGAAATCTGCT 240
 181 CAAATGTTAATTTCTTGAAGAAATCCTTCAAGCTGAGAGAGAGAAATCTGCT 240
 241 CTCAGAGGTGCTTCTGCTGCTCCGCGCGAGGCTCCAGATGATGCAAGGCTCT 300
 241 CTCAGAGGTGCTTCTGCTGCTCCGCGCGAGGCTCCAGATGATGCAAGGCTCT 300
 241 CTCAGAGGTGCTTCTGCTGCTCCGCGCGAGGCTCCAGATGATGCAAGGCTCT 300
 241 CTCAGAGGTGCTTCTGCTGCTCCGCGCGAGGCTCCAGATGATGCAAGGCTCT 300
 301 GTTCTCTCCCGGAGCTCAAGATTTCTCTCTCAAGAGAGAGAAACAGGGGATGCTT 360
 301 GTTCTCTCCCGGAGCTCAAGATTTCTCTCTCAAGAGAGAGAAACAGGGGATGCTT 360
 301 GTTCTCTCCCGGAGCTCAAGATTTCTCTCTCAAGAGAGAGAAACAGGGGATGCTT 360
 301 GTTCTCTCCCGGAGCTCAAGATTTCTCTCTCAAGAGAGAGAAACAGGGGATGCTT 360
 361 GTTGGCAAAAGCAGAGGCTCCGCTCCCAAAACCCCATGCTGATGATTAAGTTGCTC 420
 361 GTTGGCAAAAGCAGAGGCTCCGCTCCCAAAACCCCATGCTGATGATTAAGTTGCTC 420

Db 361 GTTGGCAAAAGCAGAGGCTCCGCTCCCAAAACCCCATGCTGATGATTAAGTTGCTC 420
 Qy 421 GTTGGCAAAAGCAGAGGCTCCGCTCCCAAAACCCCATGCTGATGATTAAGTTGCTC 480
 Db 421 GTTGGCAAAAGCAGAGGCTCCGCTCCCAAAACCCCATGCTGATGATTAAGTTGCTC 480
 Qy 481 GCGAGCTGGGCTTTTAAACAACTAGAGACTTCCGAGAGCTGCTGAGAGAGAGGCTGG 540
 Db 481 GCGAGCTGGGCTTTTAAACAACTAGAGACTTCCGAGAGCTGCTGAGAGAGAGGCTGG 540
 Qy 541 GGAAGAGGAGCTTCCAG 600
 Db 541 GGAAGAGGAGCTTCCAG 600
 Qy 601 GAATCTCCACATCATGCTTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 601 GAATCTCCACATCATGCTTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 660
 Qy 661 GTTCCAGAGCTTCAAAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATG 720
 Db 661 GTTCCAGAGCTTCAAAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATG 720
 Qy 721 GCTGCTCTTCCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 780
 Db 721 GCTGCTCTTCCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 780
 Qy 781 AGAAGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 840
 Db 781 AGAAGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 840
 Qy 841 GAAAGTGAAGTCTTCCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 900
 Db 841 GAAAGTGAAGTCTTCCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 900
 Qy 901 GTACGTAAACAAATAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 901 GTACGTAAACAAATAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 960
 Qy 961 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Qy 1021 ACMAAACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1021 ACMAAACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Qy 1081 TTTGGGAGCTTGAAG 1140
 Db 1081 TTTGGGAGCTTGAAG 1140
 Qy 1141 AGCAGAGCTTGAAG 1200
 Db 1141 AGCAGAGCTTGAAG 1200
 Qy 1201 CTGAGATGAGTCAAG 1260
 Db 1201 CTGAGATGAGTCAAG 1260
 Qy 1261 CCTGAGAGCTTGAAG 1320
 Db 1261 CCTGAGAGCTTGAAG 1320
 Qy 1321 GGTAGTCAATTAAG 1380
 Db 1321 GGTAGTCAATTAAG 1380
 Qy 1381 TTTAGAGTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1439
 Db 1381 TTTAGAGTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1439
 RESULT 3
 ABX77619

Wed Aug 13 15:18:49 2003

us-09-818-143-6.png

Page 4

ID	ABX77619 standard; cDNA; 1439 BP.
XX	
AC	ABX77619;
XX	
DT	09-APR-2003 (first entry)
XX	
DB	Differentially expressed breast cancer associated cDNA #114.
XX	
KW	Breast cancer; differential gene expression; BC-cDNA;
KW	breast cancer diagnosis; breast cancer monitoring;
KW	breast cancer treatment; breast cancer staging; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2002156263-A1.
XX	
PD	24-OCT-2002.
XX	
XX	
--	04-OCT-2001; 2001US-0974298.

05-OCT-2000; 2000US-238331P.
(CHEN/) CHEN H.
Chen H;
WPI; 2003-182653/18.

Claim 1, SEQ ID NO 146, 30pp; English.

PS Claim 1, SEQ ID NO 148; 30bp; English.

XX

CC The invention describes a combination of cDNAs (designated BC-cDNAs),
CC which are differentially expressed in breast cancer. The combination
CC includes 152 cDNA sequences, or their complements. The protein encoded
CC by any of these BC-cDNAs is useful for screening several molecules or
CC compounds to identify at least one ligand that specifically binds the
CC protein, producing or preparing polyclonal or monoclonal antibodies, or
CC purifying antibodies from a sample. The antibodies, which specifically
CC bind the protein differentially expressed in breast cancer is useful for
CC detecting the expression of a protein in a sample. The BC-cDNAs are
CC also useful for diagnosis, monitoring the treatment of, or staging,
CC breast cancer. This sequence represents a differentially expressed
CC breast cancer associated cDNA.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC seqdata.uspto.gov/sequence.html?docid=20020156263.

CC

Sequence 1439 BP; 392 A; 336 C; 338 G; 373 T; 0 other;

Query Match	100.0%	Score 1439;	DB 25;	Length 1439;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1439;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Qy	1	TAGTATCCCTGGTTATCACTTTGTGGTTAAAGAACCTTTGGGTCAGTCTGCCCA	60
Db	1	GAGTATCCCTGGTTATCACTTTGTGGTTAAAGAACCTTTGGGTCAGTCTGCCCA	60
Qy	61	TTCTCTTGAGAGATTAGCCCTGGCTCAGCTTTCACTCATATTCTTCCCTGCCTGAAGA	120
Db	61	TTCTCTTGAGAGATTAGCCCTGGCTCAGCTTTCACTCATATTCTTCTCTGCTGAAGA	120
Qy	121	AGAGAAAAAAGAGCAATTACCAGAAAACCCCTCCCTCCCACATGAGAGGCTTGG	180
Db	121	AGAGAAAAAAGAGCAAAATTACCAGAAAACCCCTCCCTCCCACATGAGAGGCTTGG	180
Qy	181	CAAAATGTTAATTTCTTAGAAATCCTTCAGACCTGAAGACGAGAGAAAAGAAATCGECT	240
Db	181	CAAAATGTTAATTTCTTAGAAATCCTTCAGACCTGAAGACGAGAGAAAAGAAATCGECT	240

Qy	241	CTCAGGGATGCTTTCGTGCGTCTCCCGCGCCAGAGCCCCAGACATTAAGTCAACAGGCGCTCTCT	300
Db	241	CTCAGGGATGCTTTCGTGCGTCTCCCGCGCGCAGAGCCCCAGACATTAAGTCAACAGGCGCTCTCT	300
Qy	301	GTTCCTCTCCCGGGAATCTCAGAAATTTCTCTCTCAAGGAAAGAAAACAGGGCATGCGTT	360
Db	301	GTTCCTCTCCCGGGAATCTCAGAAATTTCTCTCTCAAGGAAAGAAAACAGGGCATGCGTT	360
Qy	361	GTTCGCAAAACCGACAGGCGCGGCTCCCAAAAACCCCATGTGTGATACATTAAGTATGAGGCC	420
Db	361	GTTCGCAAAACCGACAGGCGCGGCTCCCAAAAACCCCATGTGTGATACATTAAGTATGAGGCC	420
Qy	421	GTCCCAAGGCGCTCCCGAGCGGCAAACTTAAAGACACAGGCTTTGCTGAAAACCAACATG	480
Db	421	GTCCCAAGGCGCTCCCGAGCGGCAAACTTAAAGACACAGGCTTTGCTGAAAACCAACATG	480
Qy	481	GCCAGCTGGGCTTTTAAACAACCTTAGACCTTCCGAGCTGCTGAAACAGAGCTGCG	540
Db	481	GCCAGCTGGGCTTTTAAACAACCTTAGACCTTCCGAGCTGCTGAAACAGAGCTGCG	540
Qy	541	GGAACCGGGGCTGCGCAGAGACACTCAGACGTTCCCTCATAGGCTGTGTTGGTCCCTTA	600
Db	541	GGAACCGGGGCTGCGCAGAGACACTCAGACGTTCCCTCATAGGCTGTGTTGGTCCCTTA	600
Qy	601	GAATCTCCACATCATGTCTTTCTGTGCGCTTTCTCTTGAGACACAGAAAGGGAAG	660
Db	601	GAATCTCCACATCATGTCTTTCTGTGCGCTTTCTCTTGAGACACAGAAAGGGAAG	660
Qy	661	GTTCCAGGCTCTAAAAAATGTGCTTGTGTACAGAGATGCGCTCAAAACCAATATACGCG	720
Db	661	GTTCCAGGCTCTAAAAAATGTGCTTGTGTACAGAGATGCGCTCAAAACCAATATACGCG	720
Qy	721	GCTGCGCTTTGAGGCGCAGTGAAGTCTAGCGCTCAAGGCTTTAAAGCACTTACAGAG	780
Db	721	GCTGCGCTTTGAGGCGCAGTGAAGTCTAGCGCTCAAGGCTTTAAAGCACTTACAGAG	780
Qy	781	AGAAAGCCCTAGAGCTCCGAGGTTCACTTAAAGAGCAAGCACTGGTTCTCTCTTA	840
Db	781	AGAAAGCCCTAGAGCTCCGAGGTTCACTTAAAGAGCAAGCACTGGTTCTCTCTTA	840
Qy	841	GAAGAAGGTTCTTGGCTGTATGTAGACTGGCTTCTTGAATTTTAAAGGGAAT	900
Db	841	GAAGAAGGTTCTTGGCTGTATGTAGACTGGCTTCTTGAATTTTAAAGGGAAT	900
Qy	901	GTACGTAAACAAAAATAGGCGTTGCGCTGTCAAGAGACAGACAGATGTAGATGGA	960
Db	901	GTACGTAAACAAAAATAGGCGTTGCGCTGTCAAGAGAGACAGAGATGTAGATGGA	960
Qy	961	TGAGTGAATGGAATGTATGATGAATAGATAGATGCTTTGCATTAATTCAGAGAA	1020
Db	961	TGAGTGAATGGAATGTATGATGAATAGATAGATGCTTTGCATTAATTCAGAGAA	1020
Qy	1021	ACAAAAACCAAGCTGATGGAACCAATTAATGTGAGGTCTGAGAGGGGAAGGTGCGAC	1080
Db	1021	ACAAAAACCAAGCTGATGGAACCAATTAATGTGAGGTCTGAGAGGGGAAGGTGCGAC	1080
Qy	1081	TTTGGGCAAGCTTTGAGAAACGGGTACAGAAAGTCTGTGCTGTGTCTCAGCCCTGAGACC	1140
Db	1081	TTTGGGCAAGCTTTGAGAAACGGGTACAGAAAGTCTGTGCTGTGTCTCAGCCCTGAGACC	1140
Qy	1141	AACCAATGACATTTAATTAAGCTTTAGAGCAACTCTTGACCAGAGATGCGTACCC	1200
Db	1141	AACCAATGACATTTAATTAAGCTTTAGAGCAACTCTTGACCAGAGATGCGTACCC	1200
Qy	1201	CTGAGATGAGGTCAAGCACTCTCTCAACATTCCTTCTCTCCGATGGAATACGAGCTCG	1260
Db	1201	CTGAGATGAGGTCAAGCACTCTCTCAACATTCCTTCTCTCCGATGGAATACGAGCTCG	1260
Qy	1261	CCTCGAGGCCAATCTCTCTTCCAGCAATTCATGACGCTTAAATTTCACTTCTGATCAC	1320
Db	1261	CCTCGAGGCCAATCTCTCTTCCAGCAATTCATGACGCTTAAATTTCACTTCTGATCAC	1320
Qy	1321	GGATCGTCAATAAGCCAGATTAACACTTAATGAGATATCTTTTGTATCGTTTT	1380

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: August 13, 2003, 04:30:47 ; Search time 5268.5 Seconds
(without alignments)

11173.755 Million cell updates/sec

Title: US-09-818-143-6

Perfect score: 1439

Sequence: 1 gagctcccttcgttaatca.....agaaaaaaaaaaaaa 1439

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

1 number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:.*
1: gb_da.*
2: gb_hcg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_or.*
21: em_ov.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_scs.*
28: em_un.*
29: em_vl.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
34: em_hcg_pln.*
35: em_hcg_rdi.*
36: em_hcg_mam.*
37: em_hcg_vre.*
38: em_gv.*
39: em_hlgo_hum.*
40: em_hlgo_mus.*
41: em_hlgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1114.8	91.4	1557	BC030030	BC030030 Homo sapi
2	1111.4	91.1	2017	BC049201	BC049201 Homo sapi
3	1283.6	89.2	128618	AC011485	AC011485 Homo sapi
4	1264	87.8	4772	AR220892	AR220892 Sequence
5	1263.6	87.8	5370	AB040951	AB040951 Homo sapi
6	1259.2	87.5	1943	HSMB01004	AL117499 Homo sapi
7	706.2	49.1	219026	AC144655	AC144655 Callacabu
8	629.8	43.8	633	AC440306	BD058661 Secreted
9	370.4	25.7	397	BD058661	BD058661 Secreted
10	300.4	20.9	309	AC330093	AC330093 Sequence
11	300.4	20.9	309	AC334468	AC334468 Sequence
12	165.8	11.5	620	CFRA11544	AX11544 Canis fam
13	115.4	8.0	89328	AX329823	AX329823 Sequence
14	115.4	8.0	89328	HS398C22	293784 Human DNA s
15	86.2	6.0	215105	AC073717	AC073717 Mus muscu
16	78	5.4	220731	AC097166	AC097166 Rattus no
17	78	5.4	220731	AC134186	AC134186 Rattus no
18	78	5.4	325888	AC119556	AC119556 Rattus no
19	61.6	4.3	203058	AL844150	AL844150 Zebrafish
20	61.2	4.3	197200	EX005260	EX005260 Dario rer
21	60.6	4.2	7218	166494	166494 Sequence 14
22	59.4	4.1	186752	AC019274	AC019274 Homo sapi
23	58.4	4.1	112270	AC093332	AC093332 Homo sapi
24	58.4	4.1	179844	AP002501	AP002501 Homo sapi
25	58.4	4.1	187465	AC090209	AC090209 Homo sapi
26	58.4	4.1	204623	AP001338	AP001338 Homo sapi
27	57.6	4.0	125020	AF429315	AF429315 Homo sapi
28	57	4.0	254127	AC132482	AC132482 Mus muscu
29	56.8	3.9	203817	EX248239	EX248239 Dario rer
30	56.6	3.9	63459	AC021210	AC021210 Homo sapi
31	56.6	3.9	81078	AC023588	AC023588 Homo sapi
32	56.6	3.9	185531	EX470204	EX470204 Dario rer
33	56.6	3.9	199030	AC011324	AC011324 Rattus no
34	56.6	3.9	258571	AC097144	AC097144 Rattus no
35	56.4	3.9	103019	AC091292	AC091292 Takifugu
36	56.4	3.9	154262	AC127629	AC127629 Rattus no
37	56.4	3.9	172174	EX000472	EX000472 Zebrafish
38	56.4	3.9	210483	AC111508	AC111508 Rattus no
39	56	3.9	155361	AC142174	AC142174 Rattus no
40	55.8	3.9	117721	AC093655	AC093655 Homo sapi
41	55.8	3.9	168893	EX530090	EX530090 Mus muscu
42	55.8	3.9	208360	AC020708	AC020708 Homo sapi
43	55.8	3.9	218868	AL929073	AL929073 Mus muscu
44	55.8	3.9	234288	AL772311	AL772311 Mus muscu
45	55.8	3.9	246337	AC106464	AC106464 Rattus no

ALIGNMENTS

RESULT 1
BC030030 1557 bp mRNA linear PRI 20-MAY-2002
LOCUS BC030030
DEFINITION Homo sapiens, DKFZP434N161 protein, clone MGC:3507 IMAGE:3605290,
mRNA, complete cde.
ACCESSION BC030030
VERSION BC030030.1 GI:20987193
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1557)
AUTHORS Strauberg,R.
TITLE Direct Submission

